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GTCACCGTGG	CCGGCGCTGG	CGACGCGGAC	CGGTACGGGA	TCCACCCCGC	GCTGCTGGAC	6240
GCCTCGCTCC	GCACGGTGGT	CGGCGAGGAC	CTGCTCCCGT	CGGTGTGGAC	CGGCGTGTCC	6300
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ACCGCGAATA	CCGCGGACTT	CCTGCCGTAC	GAGGCCAGCT	CGGCGAGGCG	GACCTCTCTC	6540
CGCTCCAGG	CCTGCTGGGC	AGACCCCGCG	GAAACCGGCG	TGGCGGTGGT	CACCGGGGAC	6600
TGCACCGAAC	CCGGCGCGGC	CGGATCTGG	GGCTGGTGC	GCTCGGCGCA	GTCGGAACAC	6660
CCCGGCGGGA	TGCTGCTGGC	CGACCTGAC	GACCCCGCGG	TGCTGCCCGG	CGTGTGGGCG	6720
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CTGGGGGCAT	CGTCCGCCAT	CGCGCGCTGC	GACGTGGCAG	ACCGGGGCGCA	GCTCGAAGCC	7020

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 CCTGGCCCG CGCCGGCTC GAACCGTCC ATGTGGACAT CATTGAAGGG CACGGCACCG 47400
 GGACGGCGT GGGCGACCG ATCGAGGCG AGGCCCTGCT GGCACCTAC GCGAAGGACC 47460
 GCGACCCGA GAGCCGTG TGCTGGGGT CGGTGAGTC GAACCTCGGC CACACGAGT 47520
 CGCGGGCGG CGTGCCCGG GTGATCAAGA TGTGCGAGC GCTGGCGAC GCGCTCATC 47580
 CGCCACCTT GACGTGGAC CGGCCACCA GCGAGTGA CTGCTCGCG GGGCCCGTC 47640
 AAGTCTGAC CGAGGACCG GAGTGGCCG GGAACGGCG TCCCGCCCG GCGGGGTGT 47700
 CCTGCTTGG GATCAGCGC ACQAACGCC AACTGATCAT CGAAGAGCA CCGGCCGAGC 47760
 CACAGCTTG CGACACCG CGGACGCG GTGTGCTGC GTTGTCTC TTGGCTCGCA 47820
 GCGCCGTGC CCTGGCGGT CAGGCGGTC GGTGGCCAC GTTCTCGGC GAGGGCCCC 47880
 TTTCGACCT CGCCGTTCG CTGACGAGC GCGCCCTTT CGGCGAGCG GCGGTCTCG 47940
 TCGCGATTC GCGCGAGAA GCGCGCGCG GTCTGGCGC ACTGGCCCG GCGAAGAGC 48000
 CGCGGGCTT GTTCGCGC CGGTCGCCG CTTCGGCTT GCGGGCAG CTCTGTGGG 48060
 TGTTCGCCG CGAGGGAGC CAGTGGGTG GATGGCCG CGAATCTTC GAAGAGTCTC 48120

CGGTGTTCG CGAGCGGATC GCGAGTGTG CGGCGCGCT GGAGCCGTGG ATCGGCTGGT 48180

CGGTGTTCGA CGTCTCTCTT GCGAGCGGTG ACGTGGATCG GGTGGATGTG CTGAGGCCCG 48240

CGTGTCTTGC GGTGATGGTC GCGTTGCCG CGGTGTGGTC CTGCGCGGG GTGTCTCCCG 48300

ATGCGGTGCT CGGCCACTCC CAGGTTGAGA TCGCCGCGGC GTGCTGTTCG GGTGCGTTGT 48360

CGCTGGAGGA TCGGCGAAG GTGGTTGCC TCGCGAGCA GGCATGCGC GCGAAGCTCT 48420

CCGCGCCCG CGGGATGCT TCGGTGCGCT TGGCGAAGC CGATGTGGTG TCGCGCTGG 48480

CGGACGGGT CGAGGTGGCT GCGCTCAACG GTCCGGGTC CGTGGTATC GCGGGGATG 48540

CCGAGCCCT CGAGCAAGC CTGGAAGGC TGTCTGTTC GGAATCCG GCTCGCCGG 48600

TGCGGTGGA CTACGCTCG CACACCGGC ACGTGAAGA CATCGAAGC ACCCTGCCC 48660

AAGCGCTGC CGGGATGAC GCGCGGCGC CGCTGGTGC GTTCTCTCC ACCCTACCG 48720

CGGAGTGGAT CCGGACGAG GCGCTCGTG ACGCGGCTA CTGGTACCG AACCTGCGG 48780

GCGGGTTCG GTTCCGCCG GCGCTCGAG CGCTGCTGC CAGGGGCGC GGTGTGTTCG 48840

TGAGGTGAG CGCCACCCG GTGCTGGTCC AGCGATCAC CGAGCTCAC GACGAACCG 48900

CCGCGTCTT CACCGTTTC CTGCGCGCG ACGACGCTG CTTGCGCGG CTGCTGACT 48960

CGATGGCGA GCTCTCTTC GTTGGGTTC AAGTGGACTG GAGCTGCTG GTGCGCGCG 49020

CCGCGCGCA CTTCCGAGC TACGCTTTC ACCAGAGCA CTACTGGCTC CGCGCGCGG 49080

ACACCGCTC CGACGCGTC TCGCTGGGC TGGCGGGGC GGACACCCG CTGCTCGCG 49140

CGGTGTGCA GCTTCGCG TCCGAGGCG TGGTCTTAC TTCCGCGTC TCCCTGCGT 49200

CGCACCCCTG GCTGGCCGAC CACGGGGTCC GGGAGCTCGT GATCGTCCCG GGCACCGGCG 49260
 TGGTCGAGCT GCGCGTGGCG GCCCGTGACG AAGCCGGCTG CCGCGTGCTC GACGAGCTGG 49320
 TGATCGAGGG GCGCGTCGTG GTGCCCGGCC GCGGCGGGGT CCGCGTGACG GTGCGCCCTG 49380
 GCGGCCCCCG CGACGACGGT TCGCGCACGG TGGACGTCTT CTCCTGCGC GAAGACGGCG 49440
 ACAGCTGGCT CCGGCACGCC ACGGGGCTGC TGGTCCCGGA GAACCGGCCG CGGGGACCG 49500
 CGCGGTTCGA CTTCGCGGCC TGGCGGCTAC CGGAGGCGAA GCGCTGGAG CTCACCGGTG 49560
 CCTACGACGT GCTCGGGAC GTGCGGTACG GCTACGGGCC CAGGTCGCG GCGGTGCGGG 49620
 CGGTGTGGCG GCGCGGCAGC GCGAACACCA CCGAGACCTT CCGCGAGATC GCGCTGCCCG 49680
 AAGACGCCCG CGCGGAAGCC GCGCGTTTCG GATTCGACCC CGCGCTGCTG GAGCGGGGCC 49740
 TGCACTCGAC GATGCTCAGC GCGCGCGCG ACACCGAGTC CTACCGCGAC GAAGTCGGGC 49800
 TCGCGTTGCG GTGGAACGGG CTGCGGCTGC ACGCGGCGCG CGCCTCGGTG CTGCGGCTGC 49860
 GCGTGCCCAA GCTCGAGCGG GACAGTCTGT CCGTGGAGGC CCGCGACGAG TCCGGCGGCC 49920
 TGGTCGTGAC GCTGGATTCC CTGCTCGGGC GCGCGGTGTC GAACGACCGC CTGACGACGG 49980
 CGCGGGGCC GCGGGCGGCC GCGTCGCTGT ACCCGGTGGA CTGACGCGCA TTCTCTCTAG 50040
 TCGACACTTC GGGACGGGTG CGCTCCCTGG TTCCGCTGCG CACCGCGGAA GAGGTGCGCA 50100
 CGCTGGCCGA CGAGTCTCTG ACCCGCGGGA CCGAGGCGCC GCGGTGCGCC GTCTGGAGG 50160
 CGCTCGCCGA CGAGGTTTCC GTGCTGGGCG TCACCGTCCG GGTGCTGAC GTGCTGACG 50220
 GCTGCTGCG CCGCGGCGGG CTGAGGCGGA CGAAGCTGCC GATCGTCAAC CCGCGCGCGG 50280
 TGCCCGCCGG CGAGGCGGTG GTGCAAGACC CGGCGCGCGC CAGCGGTGCG GCGCTGGTCC 50340

GGGCCCGCGCA GGCAGAGAAC CCGGACGGGA TGCTCTCTCT CGACGTCGAG CCGSAAGCCG 50400
 ACGTACCGCC GCTGCTGGGT TGGTGTCTCG CCGACGGGGA GCGCAGGTC GCGGTGCGGG 50460
 GAACCAAGCT GTCCATCCCC CGCTTCGCC GCGCGGCTCG GCCGAGCCG GCCGCGGGT 50520
 TCAGAGCCCG GGGACCGGTG CTGGTCACCG GCGGACCGG GTCGCTGGCG GCGCTGGTGG 50580
 CCGGCGACCT GGTGAGCGG CAGGGGCTTC GGCAGCTGGT GCTGGGAGT CCGCGGGGCC 50640
 TGGACGCCGA AGGCGCGAAG GACCTGGTCA CCGACCTCAC CGCACTGGGG GCCGACGTGG 50700
 CGGTGCGCC TTGCGAGCTC CCGGACCGGG ACCAGGTGGC GGGCTGTGT ACCGAGCACC 50760
 GCGCGTCCG CGTGGTGCAC ACGGCGGGG TCGCGGACGC CGGGGTGATC GGGACGGTGA 50820
 CCGCGGACCG GCTGGCGGAG GTGTTCGGC CAGAGTTCAC CGGGCGCCG CACCTCGAGC 50880
 AGCTGACCCG CGACCTGGAC CTGACAGTT TGCTCTCTA CTCTCGGTT TCGCGGTGT 50940
 TCATGGGCG CCGCAGGGC AGCTACGCC CCGCGAACGC GTACCTGGAC GGGTGTATGG 51000
 CCGACCGGG CCGCGCGCG CTGCGGGGCC AGTGGCTGGC GTGGGGCTG TGGACCGAGA 51060
 CCACCGCGG CATGGCGGC GGGACCGAG AGGCGGGCG GCGCGGATG ACCCGCGCG 51120
 GCGGCTGGT CGCGATGAAA CCGGCGCGG GACTGGACCT CTTGAGGCT GCGTCGGGT 51180
 CCGCGAGGC GCTGCTGGTG CCGGCGGAG TCGACCTGGC GGGCTGGCG GCCGAGCGG 51240
 CGGCGCGAC CGAAGTGGC CACCTGCTGC GCGGCTGGT CCGCGCGGA CGCGAGAGG 51300
 CCGGTGCGG GTTCACTGTG GAGGAGAACT GCGCGGGCG GCTGCGCGG CTCGAGCCCG 51360
 CCGAGCGGG CAGGTCTCT CTGGAACTG TCGCGGCCA GGTGGCAGG GTCTGGGCT 51420

ACCGCGCCG	CCACCAGGTC	GACCCGGAAC	AGGGCCGTGT	CGAGATCGGG	TTGACTCGCC	51480
TCACCGCGAT	CGAAGTCGCG	AAACGGGCTGC	GCGCCAGGAC	CGAACGGAAG	ATCTCGCCCG	51540
GTGTGTGCTT	CGACCATCCC	ACGCGGGCCC	TGCTCGCGCG	GCACCTTGAC	GAGCTGCTCC	51600
GAAGAAGGT	GTGAACGTGT	TCGACGTGGA	GACCTACCTC	CAGCGGATCG	GCTGCGGCGG	51660
GGAACCGGC	GTGACCTCG	AAACGCTGGC	GAAGCTGCAG	AAGAGCCACC	TGATGGCGAT	51720
CCCGTACAGC	AGCGTCGCT	ACGAACTCCG	GGACGCGGTG	AACGTGCTCG	ACCTGACGGA	51780
GGACGACCTC	TTCTACCA	GCATGCGGA	AGGGCAGGGC	GGCGCTGCT	ACCACCTGAA	51840
CCGGCTGTT	CACCGCTCC	TGACCGAAT	CGGCTACGAC	GTACGCGCG	TGCGCGGAG	51900
CACCGCGAA	GGCGGGAGA	CCTTGGGAC	CGAGTCGAG	CACATGTTCA	ACCTGGTCAC	51960
CTTGACGGC	GCGACTGGC	TGCTGGAAT	CGGCTACCC	GGCCACACT	ACGTGAGCC	52020
ACTGGCGTC	TGCGCGCGG	TGCAGACCA	GTACGGGAGC	CAGTCCGGT	TGGTGAACA	52080
GGAACCGGT	TATGCGCTC	AACCGCGGG	TGCGTCCAC	CGCTGAGCG	TGCTTACAC	52140
GTTCACGAGC	CAACCGGTC	AGTGGAGTA	CTGGAAGGAA	CTGGAGGACA	ACTTCGGGGC	52200
CTCGTGGGG	GACACCAACC	GCACCGACAC	GCAGGAACC	CTGTGCGGCC	GCGGCTTCGC	52260
GAACGGCGAG	GTCTTCTGC	GGCAGCGCG	CTACCTGAGC	GTGAGAACG	GCGCGAGCA	52320
GGTGGGACG	ATCACCGAGC	ACGACGATTT	CCGGGCGCTG	GTGTCCCGCG	TGCTGTCCGG	52380
CGACCACGGC	TGAAGTCGG	AAAGGCAAG	CGATGAGGA	AAAAGCGGGC	CTCTGGGGA	52440
AGTTCGCGG	CTCTGCAAA	ACCGCTAGG	AGCAGCACTA	CATCCGTTAC	CTGCACTTCT	52500
TTTTCGCGG	CGAGTACTTC	CACCAAGGCA	GCGAGCGGT	GTCCCGATTC	GCGGACCTGC	52560

CGTACGTGAC CGTGCCTGAG CCGCGGAAGA AGGCGCGGTG AGGACGACGA TCCCGGTCCG 52620
 CCTGGCGGAA CCGTCCCTACG ACGTGTCTGT CGGCCCCGGG GTGGCGGCGG CGCTGCCCGA 52680
 GGTCTGTCGG CCGCTGGGCG CGAGACGGGC CGTGTCTGTG TCGCCCTGGC CGCGGGACTG 52740
 GGTGCCCGGC ACCCGGCTCG AGACCCCTGCT GCTCCAGGCG CGCGACGGCG AGCGGACCAA 52800
 CGCGCTGTCC ACAGTGGAGG AACTGTGGCG TGAGTTGGCG CGGTTCGGGC TCACCCGGTC 52860
 CGACGTCTGT GTCTCTTGCG GCGGCGGCAC GAACACGGAC GTCTTCGGGC TCGCGGCCGC 52920
 GTGTACCAAC CCGGGGGTGG CCGTGTGTCA CCTGCCCAGC TCCTGTCTCG CCACGGTCCA 52980
 CGCCACCGTC GCGCGGAAGA CCGCGGTGAA CCTGCCGCGT GGCAAGAACC TCGTCGGGGC 53040
 GTACTGGCGG CCCAGCGCGG TGCTGTGCGA CACGSACTAC CTGACGACGC TCGCGCGGCG 53100
 GGAGGTGCTG AACGCGCTCG GCGAGATGCG CCGCTGCCAC TTTCTCGGCG CGCCGGACCT 53160
 GCGGGGGGCG TCGCGCCCGG AGCAGATGCG CGCCAGCGTC ACCCTCAAGG CGGGCATCGT 53220
 CGCGCAGGAC GAGCGGGACA CCGGCCCGCG GCACCTGCTC AACTACGGCC ACACGCTGGG 53280
 GCACGCGCTG GAGATCGCGA CCGGCTTGCG CCTGCGCAC GCGGAGGCGG TGGCGATCGG 53340
 CAGGCTCTTC GCGGCGCGC TGACCGGCGC GCTCGGCCG CTGACCACTT CCGTGTGGA 53400
 CGAACACCTC GCGGTGTGCG GCGCATACGG CCTGCGCGC CGCTTGCGCG CGGAAGTCCA 53460
 CGCGCGGGTG CTCTTCGCGC AGATGTACCG GGACAAGAAG GCGATCACCG GGCTGCCCTT 53520
 CGTCTGCGC GGGCGCGGG GCGCGGAGCT GGTGAGCGAC GTGCCGCGC CGGTCTCAC 53580
 CGACGTCTTG GACCGGATCG CCGCGACAG CCTGGAACAC CTGTGGGGA CGACGGAAGC 53640

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GGCGGCGCCG TGAGCGGCA GCGGACTTC GGGGCGACG GCGGGCGGT CGACCGGGTG 53700

CTGGCGGGCC GCGTGAGCG GCGCTGGCC CGGCGGCGG CGCAGCAGCC GGGCTGGCGG 53760

GACGCGGAGC GGGCGGCCGA GGTGAATTC 53789

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4572 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Phe Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys Gly Val Val Ser
1 5 10 15

Thr Gln Arg Asn Cys Leu Trp Ser Val Ala Ser Cys Tyr Val Pro Phe
20 25 30

Pro Gly Leu Ser Asp Gln Asp Arg Val Leu Trp Pro Leu Pro Leu Phe
35 40 45

His Ser Leu Ser His Ile Ala Cys Val Leu Ser Ala Thr Val Val Gly
50 55 60

Ala Ser Val Arg Ile Ala Asp Gly Ser Ser Ala Asp Asp Val Met Arg
65 70 75 80

Leu Ile Glu Ala Glu Ser Ser Thr Phe Leu Ala Gly Val Pro Thr Thr
85 90 95

Tyr His His Leu Val Arg Ala Ala Arg Gln Arg Gly Phe Ser Ala Pro
100 105 110

Ser Leu Arg Ile Gly Leu Ala Gly Gly Ala Val Leu Gly Ala Gly Leu
115 120 125

Arg Ser Glu Phe Glu Glu Thr Phe Gly Val Pro Leu Ile Asp Ala Tyr
130 135 140

Gly Ser Thr Glu Thr Cys Gly Ala Ile Thr Met Asn Pro Pro Asp Gly
145 150 155 160

Ala Arg Val Glu Gly Ser Cys Gly Leu Ala Val Pro Gly Val Asp Val
165 170 175

Arg Val Val Asp Pro Asp Thr Gly Leu Asp Val Pro Ala Gly Glu Glu
180 185 190

Gly Glu Val Trp Val Ser Gly Pro Asn Val Met Leu Gly Tyr His Asn
195 200 205

Ser Pro Glu Ala Thr Ala Ala Ala Met Arg Asp Gly Trp Phe Arg Thr
210 215 220

Gly Asp Leu Ala Arg Arg Asp Asp Ala Gly Tyr Phe Thr Ile Cys Gly
225 230 235 240

Arg Ile Lys Glu Leu Ile Ile Arg Gly Gly Ala Asn Ile His Pro Gly
245 250 255

Glu Val Glu Ala Val Leu Arg Thr Val Asp Gly Val Ala Asp Ala Ala
260 265 270

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Val Gly Gly Val Pro His Asp Thr Leu Gly Glu Val Pro Val Ala Tyr
275 280 285

Val Ile Pro Gly Pro Thr Gly Phe Asp Pro Ala Ala Leu Ile Glu Lys
290 295 300

Cys Arg Glu Gln Leu Ser Ala Tyr Lys Val Pro Asp Arg Ile Leu Glu
305 310 315 320

Val Ala His Ile Pro Arg Thr Ala Ser Gly Lys Ile Arg Arg Gly Leu
325 330 335

Leu Thr Asp Glu Pro Ala Gln Leu Arg Tyr Ala Ala Thr Glu His Glu
340 345 350

Glu Gln Ser Arg His Ala Asp Glu Ser Val Ala Ala Ala Leu Arg Ala
355 360 365

Arg Leu Ser Gly Leu Asp Glu Arg Ala Gln Cys Glu Leu Leu Glu Asp
370 375 380

Leu Val Arg Thr Gln Ala Ala Asp Val Leu Gly Gln Pro Val Pro Asp
385 390 395 400

Gly Arg Ala Phe Arg Asp Leu Gly Phe Thr Ser Leu Ala Ile Val Glu
405 410 415

Leu Arg Asn Arg Leu Thr Glu His Thr Gly Leu Trp Leu Pro Ala Ser
420 425 430

Ala Val Phe Asp His Pro Thr Pro Ala Ala Leu Ala Ala Arg Val Arg
435 440 445

Ala Glu Leu Leu Gly Ile Thr Gln Ala Val Ala Glu Pro Val Val Ala
450 455 460

Ala Asp Pro Gly Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Leu

465	470	475	480
Pro Gly Gly Val Ala Ser Pro Glu Asp Leu Trp Arg Leu Val Ala Glu			
485	490	495	
Arg Val Asp Ala Val Ser Glu Phe Pro Gly Asp Arg Gly Trp Asp Leu			
500	505	510	
Asp Ser Leu Ile Asp Pro Asp Arg Glu Arg Ala Gly Thr Ser Tyr Val			
515	520	525	
Gly Gln Gly Gly Phe Leu His Asp Ala Gly Glu Phe Asp Ala Gly Phe			
530	535	540	
Phe Gly Ile Ser Pro Arg Glu Ala Val Ala Met Asp Pro Gln Gln Arg			
545	550	555	560
Leu Leu Leu Glu Thr Ser Trp Glu Ala Leu Glu Asn Ala Gly Val Asp			
565	570	575	
Pro Ile Ala Leu Lys Gly Thr Asp Thr Gly Val Phe Ser Gly Leu Met			
580	585	590	
Gly Gln Gly Tyr Gly Ser Gly Ala Val Ala Pro Glu Leu Glu Gly Phe			
595	600	605	
Val Thr Thr Gly Val Ala Ser Ser Val Ala Ser Gly Arg Val Ser Tyr			
610	615	620	
Val Leu Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser			
625	630	635	640
Ser Ser Leu Val Ala Met His Leu Ala Ala Gln Ala Leu Arg Gln Gly			
645	650	655	
Glu Cys Ser Met Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro			
660	665	670	

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Gly Ser Phe Val Glu Phe Ser Arg Gln Arg Ala Leu Ala Pro Asp Gly
 675 680 685

Arg Cys Lys Ala Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp Ser Glu
 690 695 700

Gly Val Gly Val Val Val Leu Glu Arg Leu Ser Val Ala Arg Glu Arg
 705 710 715 720

Gly His Arg Ile Leu Ala Val Leu Arg Gly Ser Ala Val Asn Gln Asp
 725 730 735

Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Leu Ser Gln Gln Arg
 740 745 750

Val Ile Arg Arg Ala Leu Ala Ala Ala Gly Leu Ala Pro Ser Asp Val
 755 760 765

Asp Val Val Glu Ala His Gly Thr Gly Thr Thr Leu Gly Asp Pro Ile
 770 775 780

Glu Ala Gln Ala Leu Leu Ala Thr Tyr Gly Gln Glu Arg Lys Gln Pro
 785 790 795 800

Leu Trp Leu Gly Ser Leu Lys Ser Asn Ile Gly His Ala Gln Ala Ala
 805 810 815

Ala Gly Val Ala Gly Val Ile Lys Met Val Gln Ala Leu Arg His Glu
 820 825 830

Thr Leu Pro Pro Thr Leu His Val Asp Lys Pro Thr Leu Glu Val Asp
 835 840 845

Trp Ser Ala Gly Ala Ile Glu Leu Leu Thr Glu Ala Arg Ala Trp Pro
 850 855 860

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Arg Asn Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser
865 870 875 880

Gly Thr Asn Ala His Leu Ile Leu Glu Glu Ala Pro Ala Glu Glu Pro
885 890 895

Val Ala Ala Pro Glu Leu Pro Val Val Pro Leu Val Val Ser Ala Arg
900 905 910

Ser Thr Glu Ser Leu Ser Gly Gln Ala Glu Arg Leu Ala Ser Leu Leu
915 920 925

Glu Gly Asp Val Ser Leu Thr Glu Val Ala Gly Ala Leu Val Ser Arg
930 935 940

Arg Ala Val Leu Asp Glu Arg Ala Val Val Val Ala Gly Ser Arg Glu
945 950 955 960

Glu Ala Val Thr Gly Leu Arg Ala Leu Asn Thr Ala Gly Ser Gly Thr
965 970 975

Pro Gly Lys Val Val Trp Val Phe Pro Gly Gln Gly Thr Gln Trp Ala
980 985 990

Gly Met Gly Arg Glu Leu Leu Ala Glu Ser Pro Val Phe Ala Glu Arg
995 1000 1005

Ile Ala Glu Cys Ala Ala Ala Leu Ala Pro Trp Ile Asp Trp Ser Leu
1010 1015 1020

Val Asp Val Leu Arg Gly Glu Gly Asp Leu Gly Arg Val Asp Val Leu
1025 1030 1035 1040

Gln Pro Ala Cys Phe Ala Val Met Val Gly Leu Ala Ala Val Trp Glu
1045 1050 1055

Ser Val Gly Val Arg Pro Asp Ala Val Val Gly His Ser Gln Gly Glu

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1060	1065	1070
Ile Ala Ala Ala Cys Val Ser Gly Ala Leu Ser Leu Glu Asp Ala Ala		
1075	1080	1085
Lys Val Val Ala Leu Arg Ser Gln Ala Ile Ala Ala Glu Leu Ser Gly		
1090	1095	1100
Arg Gly Gly Met Ala Ser Val Ala Leu Gly Glu Asp Asp Val Val Ser		
1105	1110	1115
1120		
Arg Leu Val Asp Gly Val Glu Val Ala Ala Val Asn Gly Pro Ser Ser		
1125	1130	1135
Val Val Ile Ala Gly Asp Ala His Ala Leu Asp Ala Thr Leu Glu Ile		
1140	1145	1150
Leu Ser Gly Glu Gly Ile Arg Val Arg Arg Val Ala Val Asp Tyr Ala		
1155	1160	1165
Ser His Thr Arg His Val Glu Asp Ile Arg Asp Thr Leu Ala Glu Thr		
1170	1175	1180
Leu Ala Gly Ile Ser Ala Gln Ala Pro Ala Val Pro Phe Tyr Ser Thr		
1185	1190	1195
1200		
Val Thr Ser Glu Trp Val Arg Asp Ala Gly Val Leu Asp Gly Gly Tyr		
1205	1210	1215
Trp Tyr Arg Asn Leu Arg Asn Gln Val Arg Phe Gly Ala Ala Ala Thr		
1220	1225	1230
Ala Leu Leu Glu Gln Gly His Thr Val Phe Val Glu Val Ser Ala His		
1235	1240	1245
Pro Val Thr Val Gln Pro Leu Ser Glu Leu Thr Gly Asp Ala Ile Gly		
1250	1255	1260

Thr Leu Arg Arg Glu Asp Gly Gly Leu Arg Arg Leu Leu Ala Ser Met			
1265	1270	1275	1280
Gly Glu Leu Phe Val Arg Gly Ile Asp Val Asp Trp Thr Ala Met Val			
1285	1290	1295	
Pro Ala Ala Gly Trp Val Asp Leu Pro Thr Tyr Ala Phe Glu His Arg			
1300	1305	1310	
His Tyr Trp Leu Glu Pro Ala Glu Pro Ala Ser Ala Gly Asp Pro Leu			
1315	1320	1325	
Leu Gly Thr Val Val Ser Thr Pro Gly Ser Asp Arg Leu Thr Ala Val			
1330	1335	1340	
Ala Gln Trp Ser Arg Arg Ala Glu Pro Trp Ala Val Asp Gly Leu Val			
1345	1350	1355	1360
Pro Asn Ala Ala Leu Val Glu Ala Ala Ile Arg Leu Gly Asp Leu Ala			
1365	1370	1375	
Gly Thr Pro Val Val Gly Glu Leu Val Val Asp Ala Pro Val Val Leu			
1380	1385	1390	
Pro Arg Arg Gly Ser Arg Glu Val Gln Leu Ile Val Gly Glu Pro Gly			
1395	1400	1405	
Glu Gln Arg Arg Arg Pro Ile Glu Val Phe Ser Arg Glu Ala Asp Glu			
1410	1415	1420	
Pro Trp Thr Arg His Ala His Gly Thr Leu Ala Pro Ala Ala Ala Ala			
1425	1430	1435	1440
Val Pro Glu Pro Ala Ala Ala Gly Asp Ala Thr Asp Val Thr Val Ala			
1445	1450	1455	

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Gly Leu Arg Asp Ala Asp Arg Tyr Gly Ile His Pro Ala Leu Leu Asp
1460 1465 1470

Ala Ala Val Arg Thr Val Val Gly Asp Asp Leu Leu Pro Ser Val Trp
1475 1480 1485

Thr Gly Val Ser Leu Leu Ala Ser Gly Ala Thr Ala Val Thr Val Thr
1490 1495 1500

Pro Thr Ala Thr Gly Leu Arg Leu Thr Asp Pro Ala Gly Gln Pro Val
1505 1510 1515 1520

Leu Thr Val Glu Ser Val Arg Gly Thr Pro Phe Val Ala Glu Gln Gly
1525 1530 1535

Thr Thr Asp Ala Leu Phe Arg Val Asp Trp Pro Glu Ile Pro Leu Pro
1540 1545 1550

Thr Ala Glu Thr Ala Asp Phe Leu Pro Tyr Glu Ala Thr Ser Ala Glu
1555 1560 1565

Ala Thr Leu Ser Ala Leu Gln Ala Trp Leu Ala Asp Pro Ala Glu Thr
1570 1576 1580

Arg Leu Ala Val Val Thr Gly Asp Cys Thr Glu Pro Gly Ala Ala Ala
1585 1590 1595 1600

Ile Trp Gly Leu Val Arg Ser Ala Gln Ser Glu His Pro Gly Arg Ile
1605 1610 1615

Val	Leu	Ala	Asp	Leu	Asp	Asp	Pro	Ala	Val	Leu	Pro	Ala	Val	Val	Ala
1620							1625						1630		

Ser Gly Glu Pro Gln Val Arg Val Arg Asn Gly Val Ala Ser Val Pro
1635 1640 1645

Arg Leu Thr Arg Val Thr Pro Arg Gln Asp Ala Arg Pro Leu Asp Pro

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1650	1655	1660	
Glu Gly Thr Val Leu Ile Thr Gly Gly Thr Gly Thr Leu Gly Ala Leu			
1665	1670	1675	1680
Thr Ala Arg His Leu Val Thr Ala His Gly Val Arg His Leu Val Leu			
	1685	1690	1695
Val Ser Arg Arg Gly Glu Ala Pro Glu Leu Gln Glu Glu Leu Thr Ala			
	1700	1705	1710
Leu Gly Ala Ser Val Ala Ile Ala Ala Cys Asp Val Ala Asp Arg Ala			
	1715	1720	1725
Gln Leu Glu Ala Val Leu Arg Ala Ile Pro Ala Glu His Pro Leu Thr			
	1730	1735	1740
Ala Val Ile His Thr Ala Gly Val Leu Asp Asp Gly Val Val Thr Glu			
	1745	1750	1755
			1760
Leu Thr Pro Asp Arg Leu Ala Thr Val Arg Arg Pro Lys Val Asp Ala			
	1765	1770	1775
Ala Arg Leu Leu Asp Glu Leu Thr Arg Glu Ala Asp Leu Ala Ala Phe			
	1780	1785	1790
Val Leu Phe Ser Ser Ala Ala Gly Val Leu Gly Asn Pro Gly Gln Ala			
	1795	1800	1805
Gly Tyr Ala Ala Ala Asn Ala Glu Leu Asp Ala Leu Ala Arg Gln Arg			
	1810	1815	1820
Asn Ser Leu Asp Leu Pro Ala Val Ser Ile Ala Trp Gly Tyr Trp Ala			
	1825	1830	1835
			1840
Thr Val Ser Gly Met Thr Glu His Leu Gly Asp Ala Asp Leu Arg Arg			
	1845	1850	1855

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Asn Gln Arg Ile Gly Met Ser Gly Leu Pro Ala Asp Glu Gly Met Ala
 1860 1865 1870

Leu Leu Asp Ala Ala Ile Ala Thr Gly Gly Thr Leu Val Ala Ala Lys
 1875 1880 1885

Phe Asp Val Ala Ala Leu Arg Ala Thr Ala Lys Ala Gly Gly Pro Val
 1890 1895 1900

Pro Pro Leu Leu Arg Gly Leu Ala Pro Leu Pro Arg Arg Ala Ala Ala
 1905 1910 1915 1920

Lys Thr Ala Ser Leu Thr Glu Arg Leu Ala Gly Leu Ala Glu Thr Glu
 1925 1930 1935

Gln Ala Ala Ala Leu Leu Asp Leu Val Arg Arg His Ala Ala Glu Val
 1940 1945 1950

Leu Gly His Ser Gly Ala Glu Ser Val His Ser Gly Arg Thr Phe Lys
 1955 1960 1965

Asp Ala Gly Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu
 1970 1975 1980

Ala Ala Ala Thr Gly Leu Thr Leu Ser Pro Ala Met Ile Phe Asp Tyr
 1985 1990 1995 2000

Pro Lys Pro Pro Ala Leu Ala Asp His Leu Arg Ala Lys Leu Phe Gly
 2005 2010 2015

Ser Ala Ala Asn Arg Pro Ala Glu Ile Gly Thr Ala Ala Ala Glu Glu
 2020 2025 2030

Pro Ile Ala Ile Val Ala Met Ala Cys Arg Phe Pro Gly Gly Val His
 2035 2040 2045

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Ser Pro Glu Asp Leu Trp Arg Leu Val Ala Asp Gly Ala Asp Ala Val
 2050 2055 2060

Thr Glu Phe Pro Ala Asp Arg Gly Trp Asp Thr Asp Arg Leu Tyr His
 2065 2070 2075 2080

Glu Asp Pro Asp His Glu Gly Thr Thr Tyr Val Arg His Gly Ala Phe
 2085 2090 2095

Leu Asp Asp Ala Ala Gly Phe Asp Ala Ala Phe Phe Gly Ile Ser Pro
 2100 2105 2110

Asn Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Thr
 2115 2120 2125

Ser Trp Glu Leu Phe Glu Arg Ala Ala Ile Asp Pro Thr Thr Leu Ala
 2130 2135 2140

Gly Gln Asp Ile Gly Val Phe Ala Gly Val Asn Ser His Asp Tyr Ser
 2145 2150 2155 2160

Met Arg Met His Arg Ala Ala Gly Val Glu Gly Phe Arg Leu Thr Gly
 2165 2170 2175

Gly Ser Ala Ser Val Leu Ser Gly Arg Val Ala Tyr His Phe Gly Val
 2180 2185 2190

Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val
 2195 2200 2205

Ala Leu His Met Ala Val Gln Ala Leu Gln Arg Gly Glu Cys Ser Met
 2210 2215 2220

Ala Leu Ala Gly Gly Val Met Val Met Gly Thr Val Glu Thr Phe Val
 2225 2230 2235 2240

Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ala

2245	2250	2255
Phe Ala Asp Gly Ala Asp Gly Thr Gly Trp Ser Glu Gly Val Gly Leu		
2260	2265	2270
Leu Leu Val Glu Arg Leu Ser Glu Ala Gln Arg Arg Gly His Gln Val		
2275	2280	2285
Leu Ala Val Val Arg Gly Ser Ala Val Asn Ser Asp Gly Ala Ser Asn		
2290	2295	2300
Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Lys		
2305	2310	2315 2320
Ala Leu Ala Ala Ala Gly Leu Ser Thr Ser Asp Val Asp Ala Val Glu		
2325	2330	2335
Ala His Gly Thr Gly Thr Thr Leu Gly Asp Pro Ile Glu Ala Glu Ala		
2340	2345	2350
Leu Leu Ala Thr Tyr Gly Gln Asn Arg Glu Thr Pro Leu Trp Leu Gly		
2355	2360	2365
Ser Val Lys Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly Val Ala		
2370	2375	2380
Gly Val Ile Lys Met Val Met Ala Met Arg His Gly Val Leu Pro Arg		
2385	2390	2395 2400
Thr Leu His Val Asp Arg Pro Ser Ser Tyr Val Asp Trp Ser Ala Gly		
2405	2410	2415
Ala Val Glu Leu Leu Thr Glu Ala Arg Asp Trp Val Ser Asn Gly His		
2420	2425	2430
Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Ile Gly Gly Thr Asn Ala		
2435	2440	2445

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His Val Val Leu Glu Glu Val Ala Ala Pro Ile Thr Thr Pro Gln Pro
 2450 2455 2460

Glu Pro Ala Glu Phe Leu Val Pro Val Leu Val Ser Ala Arg Thr Ala
 2465 2470 2475 2480

Ala Gly Leu Arg Gly Gln Ala Gly Arg Leu Ala Ala Phe Leu Gly Asp
 2485 2490 2495

Arg Thr Asp Val Arg Val Pro Asp Ala Ala Tyr Ala Leu Ala Thr Thr
 2500 2505 2510

Arg Ala Gln Leu Asp His Arg Ala Val Val Leu Ala Ser Asp Arg Ala
 2515 2520 2525

Gln Leu Cys Ala Asp Leu Ala Ala Phe Gly Ser Gly Val Val Thr Gly
 2530 2535 2540

Thr Pro Val Asp Gly Lys Leu Ala Val Leu Phe Thr Gly Gln Gly Ser
 2545 2550 2555 2560

Gln Trp Ala Gly Met Gly Arg Glu Leu Ala Glu Thr Phe Pro Val Phe
 2565 2570 2575

Arg Asp Ala Phe Glu Ala Ala Cys Glu Ala Val Asp Thr His Leu Arg
 2580 2585 2590

Glu Arg Pro Leu Arg Glu Val Val Phe Asp Asp Ser Ala Leu Leu Asp
 2595 2600 2605

Gln Thr Met Tyr Thr Gln Gly Ala Leu Phe Ala Val Glu Thr Ala Leu
 2610 2615 2620

Phe Arg Leu Phe Glu Ser Trp Gly Val Arg Pro Gly Leu Leu Ala Gly
 2625 2630 2635 2640

His Ser Ile Gly Glu Leu Ala Ala Ala	His Val Ser Gly Val Leu Asp
2645	2650 2655
Leu Ala Asp Ala Gly Glu Leu Val Ala Ala Arg Gly Arg Leu Met Gln	
2660	2665 2670
Ala Leu Pro Ala Gly Gly Ala Met Val Ala Val Gln Ala Thr Glu Asp	
2675	2680 2685
Glu Val Ala Pro Leu Leu Asp Gly Thr Val Cys Val Ala Ala Val Asn	
2690	2695 2700
Gly Pro Asp Ser Val Val Leu Ser Gly Thr Glu Ala Ala Val Leu Ala	
2705	2710 2715 2720
Val Ala Asp Glu Leu Ala Gly Arg Gly Arg Lys Thr Arg Arg Leu Ala	
2725	2730 2735
Val Ser His Ala Phe His Ser Pro Leu Met Glu Pro Met Leu Asp Asp	
2740	2745 2750
Phe Arg Ala Val Ala Glu Arg Leu Thr Tyr Arg Ala Gly Ser Leu Pro	
2755	2760 2765
Val Val Ser Thr Leu Thr Gly Glu Leu Ala Ala Leu Asp Ser Pro Asp	
2770	2775 2780
Tyr Trp Val Gly Gln Val Arg Asn Ala Val Arg Phe Ser Asp Ala Val	
2785	2790 2795 2800
Thr Ala Leu Gly Ala Gln Gly Ala Ser Thr Phe Leu Glu Leu Gly Pro	
2805	2810 2815
Gly Gly Ala Leu Ala Ala Met Ala Leu Gly Thr Leu Gly Gly Pro Glu	
2820	2825 2830
Gln Ser Cys Val Ala Thr Leu Arg Lys Asn Gly Ala Gln Val Pro Asp	

2835	2840	2845
Val Leu Thr Ala Leu Ala Glu Leu His Val Arg Gly Val Gly Val Asp		
2850	2855	2860
Trp Thr Thr Val Leu Asp Glu Pro Ala Thr Ala Val Gly Thr Val Leu		
2865	2870	2875 2880
Pro Thr Tyr Ala Phe Gln His Gln Arg Phe Trp Val Asp Val Asp Glu		
2895	2890	2895
Thr Ala Ala Val Ser Val Thr Pro Pro Pro Ala Glu Pro Ile Val Asp		
2900	2905	2910
Arg Pro Val Gln Asp Val Leu Glu Leu Val Arg Glu Ser Ala Ala Val		
2915	2920	2925
Val Leu Gly His Arg Asp Ala Gly Ser Phe Asp Leu Asp Arg Ser Phe		
2930	2935	2940
Lys Asp His Gly Phe Asp Ser Leu Ser Ala Val Lys Leu Arg Asn Arg		
2945	2950	2955 2960
Leu Arg Asp Phe Thr Gly Val Glu Leu Pro Ser Thr Leu Ile Phe Asp		
2965	2970	2975
Tyr Pro Asn Pro Ala Val Leu Ala Asp His Leu Arg Ala Glu Leu Leu		
2980	2985	2990
Gly Glu Arg Pro Ala Ala Pro Ala Pro Val Thr Arg Asp Val Ser Asp		
2995	3000	3005
Glu Pro Ile Ala Ile Val Gly Met Ser Thr Arg Leu Pro Gly Gly Ala		
3010	3015	3020
Asp Ser Pro Glu Glu Leu Trp Lys Leu Val Ala Glu Gly Arg Asp Ala		
3025	3030	3035 3040

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Val Ser Gly Phe Pro Val Asp Arg Gly Trp Asp Leu Asp Gly Leu Tyr
 3045 3050 3055

His Pro Asp Pro Ala His Ala Gly Thr Ser Tyr Thr Arg Ser Gly Gly
 3060 3065 3070

Phe Leu His Asp Ala Ala Gln Phe Asp Ala Gly Leu Phe Gly Ile Ser
 3075 3080 3085

Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu
 3090 3095 3100

Thr Ser Trp Glu Ala Leu Glu Arg Ala Gly Val Asp Pro Leu Ser Ala
 3105 3110 3115 3120

Arg Gly Ser Asp Val Gly Val Phe Thr Gly Ile Val His His Asp Tyr
 3125 3130 3135

Val Thr Arg Leu Arg Glu Val Pro Glu Asp Val Gln Gly Tyr Thr Met
 3140 3145 3150

Thr Gly Thr Ala Ser Ser Val Ala Ser Gly Arg Val Ala Tyr Val Phe
 3155 3160 3165

Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser
 3170 3175 3180

Leu Val Ala Met His Leu Ala Ala Gln Ala Leu Arg Gln Gly Glu Cys
 3185 3190 3195 3200

Ser Met Ala Leu Ala Gly Gly Ala Thr Val Met Ala Ser Pro Asp Ala
 3205 3210 3215

Phe Leu Glu Phe Ser Arg Gln Arg Gly Leu Ser Ala Asp Gly Arg Cys
 3220 3225 3230

Lys Ala Tyr Ala Glu Gly Ala Asp Gly Thr Gly Trp Ala Glu Gly Val
 3235 3240 3245

Gly Val Val Val Leu Glu Arg Leu Ser Val Ala Arg Glu Arg Gly His
 3250 3255 3260

Arg Val Leu Ala Val Leu Arg Gly Ser Ala Val Asn Gln Asp Gly Ala
 3265 3270 3275 3280

Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val Ile
 3285 3290 3295

Arg Gly Ala Leu Ala Ser Ala Gly Leu Ala Pro Ser Asp Val Asp Val
 3300 3305 3310

Val Glu Gly His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu Val
 3315 3320 3325

Gln Ala Leu Leu Ala Thr Tyr Gly Gln Glu Arg Glu Gln Pro Leu Trp
 3330 3335 3340

Leu Gly Ser Leu Lys Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly
 3345 3350 3355 3360

Val Val Gly Val Ile Lys Met Ile Met Ala Met Arg His Gly Val Met
 3365 3370 3375

Pro Ala Thr Leu His Val Asp Glu Arg Thr Ser Gln Val Asp Trp Ser
 3380 3385 3390

Ala Gly Ala Ile Glu Val Leu Thr Glu Ala Arg Glu Trp Pro Arg Thr
 3395 3400 3405

Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Ala Ser Gly Thr
 3410 3415 3420

Asn Ala His Leu Ile Ile Glu Glu Gly Pro Ala Glu Glu Ala Val Asp

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3425	3430	3435	3440
Glu Glu Val Ala Ser Val Val Pro Leu Val Val Ser Ala Arg Ser Ala			
3445	3450	3455	
Gly Ser Leu Ala Gly Gln Ala Gly Arg Leu Ala Ala Val Leu Glu Asn			
3460	3465	3470	
Glu Ser Leu Ala Gly Val Ala Gly Ala Leu Val Ser Gly Arg Ala Thr			
3475	3480	3485	
Leu Asn Glu Arg Ala Val Val Ile Ala Gly Ser Arg Asp Glu Ala Gln			
3490	3495	3500	
Asp Gly Leu Gln Ala Leu Ala Arg Gly Glu Asn Ala Pro Gly Val Val			
3505	3510	3515	3520
Thr Gly Thr Ala Gly Lys Pro Gly Lys Val Val Trp Val Phe Pro Gly			
3525	3530	3535	
Gln Gly Ser Gln Trp Met Gly Met Gly Arg Asp Leu Leu Asp Ser Ser			
3540	3545	3550	
Pro Val Phe Ala Ala Arg Ile Lys Glu Cys Ala Ala Ala Leu Glu Gln			
3555	3560	3565	
Trp Thr Asp Trp Ser Leu Leu Asp Val Leu Arg Gly Asp Ala Asp Leu			
3570	3575	3580	
Leu Asp Arg Val Asp Val Val Gln Pro Ala Ser Phe Ala Met Met Val			
3585	3590	3595	3600
Gly Leu Ala Ala Val Trp Thr Ser Leu Gly Val Thr Pro Asp Ala Val			
3605	3610	3615	
Leu Gly His Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ser Gly Ala			
3620	3625	3630	

Leu Ser Leu Asp Asp Ala Ala Lys Val Val Ala Leu Arg Ser Gln Ala
 3635 3640 3645

Ile Ala Gly Glu Leu Ala Gly Arg Gly Gly Met Ala Ser Val Ala Leu
 3650 3655 3660

Ser Glu Glu Asp Ala Val Ala Arg Leu Thr Pro Trp Ala Asn Arg Val
 3665 3670 3675 3680

Glu Val Ala Ala Val Asn Ser Pro Ser Ser Val Val Ile Ala Gly Asp
 3685 3690 3695

Ala Gln Ala Leu Asp Glu Ala Leu Glu Ala Leu Ala Gly Asp Gly Val
 3700 3705 3710

Arg Val Arg Arg Val Ala Val Asp Tyr Ala Ser His Thr Arg His Val
 3715 3720 3725

Glu Ala Ile Ala Glu Thr Leu Ala Lys Thr Leu Ala Gly Ile Asp Ala
 3730 3735 3740

Arg Val Pro Ala Ile Pro Phe Tyr Ser Thr Val Leu Gly Thr Trp Ile
 3745 3750 3755 3760

Glu Gln Ala Val Val Asp Ala Gly Tyr Trp Tyr Arg Asn Leu Arg Gln
 3765 3770 3775

Gln Val Arg Phe Gly Pro Ser Val Ala Asp Leu Ala Gly Leu Gly His
 3780 3785 3790

Thr Val Phe Val Glu Ile Ser Ala His Pro Val Leu Val Gln Pro Leu
 3795 3800 3805

Ser Glu Ile Ser Asp Asp Ala Val Val Thr Gly Ser Leu Arg Arg Asp
 3810 3815 3820

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Asp Gly Gly Leu Arg Arg Leu Leu Ala Ser Ala Ala Glu Leu Tyr Val			
3825	3830	3835	3840
Arg Gly Val Ala Val Asp Trp Thr Ala Ala Val Pro Ala Ala Gly Trp			
	3845	3850	3855
Val Asp Leu Pro Thr Tyr Ala Phe Asp Arg Arg His Phe Trp Leu His			
	3860	3865	3870
Glu Ala Glu Thr Ala Glu Ala Ala Glu Gly Met Asp Gly Glu Phe Trp			
	3875	3880	3885
Thr Ala Ile Glu Gln Ser Asp Val Asp Ser Leu Ala Glu Leu Leu Glu			
	3890	3895	3900
Leu Val Pro Glu Gln Arg Gly Ala Leu Ser Thr Val Val Pro Val Leu			
	3905	3910	3915
Ala Gln Trp Arg Asp Arg Arg Arg Glu Arg Ser Thr Ala Glu Lys Leu			
	3925	3930	3935
Arg Tyr Gln Val Thr Trp Gln Pro Leu Glu Arg Glu Ala Ala Gly Val			
	3940	3945	3950
Pro Gly Gly Arg Trp Leu Ala Val Val Pro Ala Gly Thr Thr Asp Ala			
	3955	3960	3965
Leu Leu Lys Glu Leu Thr Gly Gln Gly Leu Asp Ile Val Arg Leu Glu			
	3970	3975	3980
Ile Glu Glu Ala Ser Arg Ala Gln Leu Ala Glu Gln Leu Arg Asn Val			
	3985	3990	3995
Leu Ala Glu His Asp Leu Thr Gly Val Leu Ser Leu Leu Ala Leu Asp			
	4005	4010	4015
Gly Gly Pro Ala Asp Ala Ala Glu Ile Thr Ala Ser Thr Leu Ala Leu			

4020	4025	4030
Val Gln Ala Leu Gly Asp Thr Thr Thr Ser Ala Pro Leu Trp Cys Leu		
4035	4040	4045
Thr Ser Gly Ala Val Asn Ile Gly Ile Gln Asp Ala Val Thr Ala Pro		
4050	4055	4060
Ala Gln Ala Ala Val Trp Gly Leu Gly Arg Ala Val Ala Leu Glu Arg		
4065	4070	4075 4080
Leu Asp Arg Trp Gly Gly Leu Val Asp Leu Pro Ala Ala Ile Asp Ala		
4085	4090	4095
Arg Thr Ala Gln Ala Leu Leu Gly Val Leu Asn Gly Ala Ala Gly Glu		
4100	4105	4110
Asp Gln Leu Ala Val Arg Arg Ser Gly Val Tyr Arg Arg Arg Leu Val		
4115	4120	4125
Arg Lys Pro Val Pro Glu Ser Ala Thr Ser Arg Trp Glu Pro Arg Gly		
4130	4135	4140
Thr Val Leu Val Thr Gly Gly Ala Glu Gly Leu Gly Arg His Ala Ser		
4145	4150	4155 4160
Val Trp Leu Ala Gln Ser Gly Ala Glu Arg Leu Ile Val Thr Gly Thr		
4165	4170	4175
Asp Gly Val Asp Glu Leu Thr Ala Glu Leu Ala Glu Phe Gly Thr Thr		
4180	4185	4190
Val Glu Phe Cys Ala Asp Thr Asp Arg Asp Ala Ile Ala Gln Leu Val		
4195	4200	4205
Ala Asp Ser Glu Val Thr Ala Val Val His Ala Ala Asp Ile Ala Gln		
4210	4215	4220

Thr Ser Ser Val Asp Asp Thr Gly Val Ala Asp Leu Asp Glu Val Phe			
4225	4230	4235	4240
Ala Ala Lys Val Thr Thr Ala Val Trp Leu Asp Gln Leu Phe Glu Asp			
	4245	4250	4255
Thr Pro Leu Asp Ala Phe Val Val Phe Ser Ser Ile Ala Gly Ile Trp			
	4260	4265	4270
Gly Gly Gly Gly Gln Gly Pro Ala Gly Ala Ala Asn Ala Val Leu Asp			
	4275	4280	4285
Ala Leu Val Glu Trp Arg Arg Ala Arg Gly Leu Lys Ala Thr Ser Ile			
	4290	4295	4300
Ala Trp Gly Ala Leu Asp Gln Ile Gly Ile Gly Met Asp Glu Ala Ala			
4305	4310	4315	4320
Leu Ala Gln Leu Arg Arg Arg Gly Val Ile Pro Met Ala Pro Pro Leu			
	4325	4330	4335
Ala Val Thr Ala Met Val Gln Ala Val Ala Gly Asn Glu Lys Ala Val			
	4340	4345	4350
Ala Val Ala Asp Met Asp Trp Ala Ala Phe Ile Pro Ala Phe Thr Ser			
	4355	4360	4365
Val Arg Pro Ser Pro Leu Phe Ala Asp Leu Pro Glu Ala Lys Ala Ile			
	4370	4375	4380
Leu Arg Ala Ala Gln Asp Asp Gly Glu Asp Gly Asp Thr Ala Ser Ser			
4385	4390	4395	4400
Leu Ala Asp Ser Leu Arg Ala Val Pro Asp Ala Glu Gln Asn Arg Ile			
	4405	4410	4415

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Leu Leu Lys Leu Val Arg Gly His Ala Ser Thr Val Leu Gly His Ser
4420 4425 4430

Gly Ala Glu Gly Ile Gly Pro Arg Gln Ala Phe Gln Glu Val Gly Phe
4435 4440 4445

Asp Ser Leu Ala Ala Val Asn Leu Arg Asn Ser Leu His Ala Ala Thr
4450 4455 4460

Gly Leu Arg Leu Pro Ala Thr Leu Ile Phe Asp Tyr Pro Thr Pro Glu
4465 4470 4475 4480

Ala Leu Val Gly Tyr Leu Arg Val Glu Leu Leu Arg Glu Ala Asp Asp
4485 4490 4495

Gly Leu Asp Gly Arg Glu Asp Asp Leu Arg Arg Val Leu Ala Ala Val
4500 4505 4510

Pro Phe Ala Arg Phe Lys Glu Ala Gly Val Leu Asp Thr Leu Leu Gly
4515 4520 4525

Leu Ala Asp Thr Gly Thr Glu Pro Gly Thr Asp Ala Glu Thr Thr Glu
4530 4535 4540

Ala Ala Pro Ala Ala Asp Asp Ala Glu Leu Ile Asp Ala Leu Asp Ile
4545 4550 4555 4560

Ser Gly Leu Val Gln Arg Ala Leu Gly Gln Thr Ser
4565 4570

(2) INFORMATION FOR SEQ ID NO: 5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5069 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5.

Met Ala Asn Gln Ser Trp Arg Lys Asn Met Ser Ala Pro Asn Glu Gln
1 5 10 15

Ile Val Asp Ala Leu Arg Ala Ser Leu Lys Glu Asn Val Arg Leu Gln
20 25 30

Gln Glu Asn Ser Ala Leu Ala Ala Ala Ala Ala Glu Pro Val Ala Ile
35 40 45

Val Ser Met Ala Cys Arg Tyr Ala Gly Gly Ile Arg Gly Pro Glu Asp
50 55 60

Phe Trp Arg Val Val Ser Glu Gly Ala Asp Val Tyr Thr Gly Phe Pro
65 70 75 80

Ser Asp Arg Gly Trp Asp Val Glu Gly Leu Tyr His Pro Asp Pro Asp
85 90 95

Asn Pro Gly Thr Thr Tyr Val Arg Glu Gly Ala Phe Leu Gln Asp Ala
100 105 110

Ala Gln Phe Asp Ala Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu
115 120 125

Ala Met Asp Pro Gln Gln Arg Gln Leu Leu Glu Val Ser Trp Glu Thr
130 135 140

Leu Glu Arg Ala Gly Ile Asp Pro His Ser Val Arg Gly Ser Asp Ile
145 150 155 160

Gly Val Tyr Ala Gly Val Val His Gln Asp Tyr Ala Pro Asp Leu Ser			
165	170	175	
Gly Phe Glu Gly Phe Met Ser Leu Glu Arg Ala Leu Gly Thr Ala Gly			
180	185	190	
Gly Val Ala Ser Gly Arg Val Ala Tyr Thr Leu Gly Leu Glu Gly Pro			
195	200	205	
Ala Val Thr Val Asp Thr Met Cys Ser Ser Ser Leu Val Ala Ile His			
210	215	220	
Leu Ala Ala Gln Ala Leu Arg Arg Gly Glu Cys Ser Met Ala Leu Ala			
225	230	235	240
Gly Gly Ser Thr Val Met Ala Thr Pro Gly Gly Phe Val Gly Phe Ala			
245	250	255	
Arg Gln Arg Ala Leu Ala Phe Asp Gly Arg Cys Lys Ser Tyr Ala Ala			
260	265	270	
Ala Ala Asp Gly Ser Gly Trp Ala Glu Gly Val Gly Val Leu Leu Leu			
275	280	285	
Glu Arg Leu Ser Val Ala Arg Glu Arg Gly His Gln Val Leu Ala Val			
290	295	300	
Ile Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr			
305	310	315	320
Ala Pro Asn Gly Pro Ala Gln Gln Arg Val Ile Arg Lys Ala Leu Ala			
325	330	335	
Ser Ala Gly Leu Thr Pro Ser Asp Val Asp Thr Val Glu Gly His Gly			
340	345	350	

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Thr Gly Thr Val Leu Gly Asp Pro Ile Glu Val Gln Ala Leu Leu Ala
 355 360 365

Thr Tyr Gly Gln Gly Arg Asp Pro Gln Gln Pro Leu Trp Leu Gly Ser
 370 375 380

Val Lys Ser Val Val Gly His Thr Gln Ala Ala Ser Gly Val Ala Gly
 385 390 395 400

Val Ile Lys Met Val Gln Ser Leu Arg His Gly Gln Leu Pro Ala Thr
 405 410 415

Gln His Val Asp Ala Pro Thr Pro Gln Val Asp Trp Ser Ala Gly Ala
 420 425 430

Ile Glu Leu Leu Ala Glu Gly Arg Glu Trp Pro Arg Asn Gly His Pro
 435 440 445

Arg Arg Gly Gly Ile Ser Ser Phe Gly Ala Ser Gly Thr Asn Ala His
 450 455 460

Met Ile Leu Glu Glu Ala Pro Glu Asp Glu Pro Val Thr Glu Ala Pro
 465 470 475 480

Ala Pro Thr Gly Val Val Pro Leu Val Val Ser Ala Ala Thr Ala Ala
 485 490 495

Ser Leu Ala Ala Gln Ala Gly Arg Leu Ala Glu Val Gly Asp Val Ser
 500 505 510

Leu Ala Asp Val Ala Gly Thr Leu Val Ser Gly Arg Ala Met Leu Ser
 515 520 525

Glu Arg Ala Val Val Val Ala Gly Ser His Glu Glu Ala Val Thr Gly
 530 535 540

Leu Arg Ala Leu Ala Arg Gly Glu Ser Ala Pro Gly Leu Leu Ser Gly

545	550	555	560
Arg Gly Ser Gly Val Pro Gly Lys Val Val Trp Val Phe Pro Gly Gln			
565	570	575	
Gly Thr Gln Trp Ala Gly Met Gly Arg Glu Leu Leu Asp Ser Ser Glu			
580	585	590	
Val Phe Ala Ala Arg Ile Ala Glu Cys Glu Thr Ala Leu Gly Arg Trp			
595	600	605	
Val Asp Trp Ser Leu Thr Asp Val Leu Arg Gly Glu Ala Asp Leu Leu			
610	615	620	
Asp Arg Val Asp Val Val Gln Pro Ala Ser Phe Ala Val Met Val Gly			
625	630	635	640
Leu Ala Ala Val Trp Ala Ser Leu Gly Val Glu Pro Glu Ala Val Val			
645	650	655	
Gly His Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ser Gly Ala Leu			
660	665	670	
Ser Leu Glu Asp Ala Ala Lys Val Val Ala Leu Arg Ser Gln Ala Ile			
675	680	685	
Ala Ala Ser Leu Ala Gly Arg Gly Gly Met Ala Ser Val Ala Leu Ser			
690	695	700	
Glu Glu Asp Ala Thr Ala Arg Leu Glu Pro Trp Ala Gly Arg Val Glu			
705	710	715	720
Val Ala Ala Val Asn Gly Pro Thr Ser Val Val Ile Ala Gly Asp Ala			
725	730	735	
Glu Ala Leu Asp Glu Ala Leu Asp Ala Leu Asp Asp Gln Gly Val Arg			
740	745	750	

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Ile Arg Arg Val Ala Val Asp Tyr Ala Ser His Thr Arg His Val Glu
755 760 765

Ala Ala Arg Asp Ala Leu Ala Glu Met Leu Gly Gly Ile Arg Ala Gln
770 775 780

Ala Pro Glu Val Pro Phe Tyr Ser Thr Val Thr Gly Gly Trp Val Glu
785 790 795 800

Asp Ala Gly Val Leu Asp Gly Gly Tyr Trp Tyr Arg Asn Leu Arg Arg
805 810 815

Gln Val Arg Phe Gly Pro Ala Val Ala Glu Leu Ile Glu Gln Gly His
820 825 830

Arg Val Phe Val Glu Val Ser Ala His Pro Val Leu Val Gln Pro Ile
835 840 845

Asn Glu Leu Val Asp Asp Thr Glu Ala Val Val Thr Gly Thr Leu Arg
850 855 860

Arg Gln Asp Gly Gly Leu Arg Arg Leu Leu Ala Ser Ala Ala Glu Leu
865 870 875 880

Phe Val Arg Gly Val Thr Val Asp Trp Ser Gly Val Leu Pro Pro Ser
885 890 895

Arg Arg Val Glu Leu Pro Thr Tyr Ala Phe Asp His Gln His Tyr Trp
900 905 910

Leu Gln Met Gly Gly Ser Ala Thr Asp Ala Val Ser Leu Gly Leu Ala
915 920 925

Gly Ala Asp His Pro Leu Leu Gly Ala Val Val Pro Leu Pro Gln Ser
930 935 940

Asp Gly Leu Val Phe Thr Ser Arg Leu Ser Leu Lys Ser His Pro Trp
 945 950 955 960

Leu Ala Gly His Ala Ile Gly Gly Val Val Leu Ile Pro Gly Thr Val
 965 970 975

Tyr Val Asp Leu Ala Leu Arg Ala Gly Asp Glu Leu Gly Phe Gly Val
 980 985 990

Leu Glu Glu Leu Val Ile Glu Ala Pro Leu Val Leu Gly Glu Arg Gly
 995 1000 1005

Gly Val Arg Val Gln Val Ala Val Ser Gly Pro Asn Glu Thr Gly Ser
 1010 1015 1020

Arg Ala Val Asp Val Phe Ser Met Arg Glu Asp Gly Asp Glu Trp Thr
 1025 1030 1035 1040

Arg His Ala Thr Gly Leu Leu Gly Ala Ser Thr Ser Arg Glu Pro Ser
 1045 1050 1055

Arg Phe Asp Phe Ala Ala Trp Pro Pro Ala Gly Ala Glu Pro Ile Asp
 1060 1065 1070

Val Glu Asn Phe Tyr Thr Asp Leu Thr Glu Arg Gly Tyr Ala Tyr Ser
 1075 1080 1085

Gly Ala Phe Gln Gly Met Arg Ala Val Trp Arg Arg Gly Asp Glu Val
 1090 1095 1100

Phe Ala Gln Val Ala Leu Pro Asp Asp His Arg Glu Asp Ala Gly Lys
 1105 1110 1115 1120

Phe Gly Leu His Pro Ala Leu Leu Asp Ala Ala Leu His Thr Asn Ala
 1125 1130 1135

Phe Ala Asn Pro Asp Asp Asp Arg Ser Val Leu Pro Phe Ala Trp Asn

1140	1145	1150
Gly Leu Val Leu His Ala Val Gly Ala Ser Ala Leu Arg Val Arg Val		
1155	1160	1165
Ala Pro Gly Gly Pro Asp Ala Leu Thr Phe Gln Ala Ala Asp Glu Thr		
1170	1175	1180
Gly Gly Leu Val Val Thr Met Asp Ser Leu Val Ser Arg Glu Val Ser		
1185	1190	1195
		1200
Ala Ala Gln Leu Glu Thr Ala Ala Gly Glu Glu Arg Asp Ser Leu Phe		
1205	1210	1215
Gln Val Asp Trp Ile Glu Val Pro Ala Thr Glu Thr Ala Ala Thr Glu		
1220	1225	1230
His Ala Glu Val Leu Glu Ala Phe Gly Glu Ala Ala Pro Leu Glu Leu		
1235	1240	1245
Thr Ser Arg Val Leu Glu Ala Val Gln Ser Trp Leu Ala Asp Ala Ala		
1250	1255	1260
Asp Glu Ala Arg Leu Val Val Val Thr Arg Gly Ala Val Arg Glu Val		
1265	1270	1275
		1280
Thr Asp Pro Ala Gly Ala Ala Val Trp Gly Leu Val Arg Ala Ala Gln		
1285	1290	1295
Ala Glu Asn Pro Gly Arg Ile Ile Leu Val Asp Thr Asp Gly Asp Val		
1300	1305	1310
Pro Leu Gly Ala Val Leu Ala Ser Gly Glu Pro Gln Leu Ala Val Arg		
1315	1320	1325
Gly Asn Ala Phe Ser Val Pro Arg Leu Ala Arg Ala Thr Gly Glu Val		
1330	1335	1340